



## SEQUENCE LISTING

<110> ALBERTSEN, MARC  
FOX, TIM  
HUFFMAN, GARY  
TRIMNELL, MARY

<120> NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND  
METHOD OF USING SAME

<130> PHI 1147

<140> 10/058,566

<141> 2002-01-28

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1197

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (2)..(991)

<400> 1

g gtg acc tca agc aag ggc aag gta tgc gta acc ggg gcc tca ggc ttt 49  
Val Thr Ser Ser Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe  
1 5 10 15

gtt gcc tct tgg ctt atc aaa cgg ctc ctc gag tct gga tat cat gtg 97  
Val Ala Ser Trp Leu Ile Lys Arg Leu Leu Glu Ser Gly Tyr His Val  
20 25 30

gta ggg act gtc agg gac cca gga aat cac caa aaa aca gcc cac ctt 145  
Val Gly Thr Val Arg Asp Pro Gly Asn His Gln Lys Thr Ala His Leu  
35 40 45

tgg aaa tta cct ggc gct aaa gag agg ctg caa atc gtg cga gct aat 193  
Trp Lys Leu Pro Gly Ala Lys Glu Arg Leu Gln Ile Val Arg Ala Asn  
50 55 60

ctg ttg gaa gaa ggg agc ttc gac agc gcc gtg atg gcc tgt gag ggt 241  
Leu Leu Glu Glu Gly Ser Phe Asp Ser Ala Val Met Ala Cys Glu Gly  
65 70 75 80

gta ttc cac act gca tcc ccc gtc ctc gct aaa ccc gac tct act agc 289  
Val Phe His Thr Ala Ser Pro Val Leu Ala Lys Pro Asp Ser Thr Ser  
85 90 95

aag gag gac acg ctc gtc cct gcg gtg aac ggt act ctg aac gtg ctg 337  
Lys Glu Asp Thr Leu Val Pro Ala Val Asn Gly Thr Leu Asn Val Leu  
100 105 110

aga tcg tgc aag aag aac ccc ttc ctg aaa agg gtc gtc ctt acg tct	385
Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Val Val Leu Thr Ser	
115 120 125	
tcg tcg tct gcg gtg agg atc agg gac gac ggt ggc cag tcc agt aac	433
Ser Ser Ser Ala Val Arg Ile Arg Asp Asp Gly Gly Gln Ser Ser Asn	
130 135 140	
atc tcg ctg gac gaa acg aca tgg agc tcc gtg cca ctc tgc gag aag	481
Ile Ser Leu Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys	
145 150 155 160	
atg cat cta tgg tat gcc cta gcc aag gta ttt gca gag aaa gcg gcg	529
Met His Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala	
165 170 175	
tgg gag ttc gcc aag gag aac ggc atc gac ctt gtg act gtc ctc ccg	577
Trp Glu Phe Ala Lys Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro	
180 185 190	
tcg ttc gtg atc ggg ccc agt ttg tcc cac gag cta tgc gtt acc gct	625
Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Val Thr Ala	
195 200 205	
tca gac gtc cta ggc cta ttc caa ggc gac acg gca agg ttc agc tcg	673
Ser Asp Val Leu Gly Leu Phe Gln Gly Asp Thr Ala Arg Phe Ser Ser	
210 215 220	
tac gga aga atg ggg tac gtc cac atc gac gac gtt gcg agc agc cac	721
Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Ser Ser His	
225 230 235 240	
atc ctg gtg tac gag gtc ccc cag gcc gcc ggg agg tac ctg tgc agc	769
Ile Leu Val Tyr Glu Val Pro Gln Ala Ala Gly Arg Tyr Leu Cys Ser	
245 250 255	
tca gtg gtg ctg gac aac gac gag ctg gtc tcc tcg ctc gcg aaa cgc	817
Ser Val Val Leu Asp Asn Asp Glu Leu Val Ser Ser Leu Ala Lys Arg	
260 265 270	
tac ccg ata ttc ccc ata ccc cgg agg ctg aac agc ccc tac ggc aag	865
Tyr Pro Ile Phe Pro Ile Pro Arg Arg Leu Asn Ser Pro Tyr Gly Lys	
275 280 285	
cag tcg tac cag ctg aac acg tcg aag ctg cag ggg ctg ggc ttc aag	913
Gln Ser Tyr Gln Leu Asn Thr Ser Lys Leu Gln Gly Leu Gly Phe Lys	
290 295 300	
ttc aga ggg gtg cag gag atg ttc gac gac tgc gtg cag tcg ctc aaa	961
Phe Arg Gly Val Gln Glu Met Phe Asp Asp Cys Val Gln Ser Leu Lys	
305 310 315 320	
gac cag ggc cac ctg ctg gag tgc ccc ctg tgaactgcga tgggggtgcc	1011
Asp Gln Gly His Leu Leu Glu Cys Pro Leu	
325 330	
tcctgtgaac gcccgttttt tttttcttc aataattcca cgtcatgtca cgggtgtctc	1071

gcgcagactg ctactgtcag gtgtcagggc gtcatagctc acgggctcta cggctacatg 1131  
 aataaaatgt cacgctagct cgtcatttgc ttgtccattt aaaaaaaaaa aaaaaaaaaa 1191  
 ctcgag 1197

<210> 2  
 <211> 330  
 <212> PRT  
 <213> Zea mays

<400> 2  
 Val Thr Ser Ser Lys Gly Lys Val Cys Val Thr Gly Ala Ser Gly Phe  
 1 5 10 15  
 Val Ala Ser Trp Leu Ile Lys Arg Leu Leu Glu Ser Gly Tyr His Val  
 20 25 30  
 Val Gly Thr Val Arg Asp Pro Gly Asn His Gln Lys Thr Ala His Leu  
 35 40 45  
 Trp Lys Leu Pro Gly Ala Lys Glu Arg Leu Gln Ile Val Arg Ala Asn  
 50 55 60  
 Leu Leu Glu Glu Gly Ser Phe Asp Ser Ala Val Met Ala Cys Glu Gly  
 65 70 75 80  
 Val Phe His Thr Ala Ser Pro Val Leu Ala Lys Pro Asp Ser Thr Ser  
 85 90 95  
 Lys Glu Asp Thr Leu Val Pro Ala Val Asn Gly Thr Leu Asn Val Leu  
 100 105 110  
 Arg Ser Cys Lys Lys Asn Pro Phe Leu Lys Arg Val Val Leu Thr Ser  
 115 120 125  
 Ser Ser Ser Ala Val Arg Ile Arg Asp Asp Gly Gly Gln Ser Ser Asn  
 130 135 140  
 Ile Ser Leu Asp Glu Thr Thr Trp Ser Ser Val Pro Leu Cys Glu Lys  
 145 150 155 160  
 Met His Leu Trp Tyr Ala Leu Ala Lys Val Phe Ala Glu Lys Ala Ala  
 165 170 175  
 Trp Glu Phe Ala Lys Glu Asn Gly Ile Asp Leu Val Thr Val Leu Pro  
 180 185 190  
 Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu Leu Cys Val Thr Ala  
 195 200 205  
 Ser Asp Val Leu Gly Leu Phe Gln Gly Asp Thr Ala Arg Phe Ser Ser  
 210 215 220  
 Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp Val Ala Ser Ser His  
 225 230 235 240

Ile Leu Val Tyr Glu Val Pro Gln Ala Ala Gly Arg Tyr Leu Cys Ser  
245 250 255

Ser Val Val Leu Asp Asn Asp Glu Leu Val Ser Ser Leu Ala Lys Arg  
260 265 270

Tyr Pro Ile Phe Pro Ile Pro Arg Arg Leu Asn Ser Pro Tyr Gly Lys  
275 280 285

Gln Ser Tyr Gln Leu Asn Thr Ser Lys Leu Gln Gly Leu Gly Phe Lys  
290 295 300

Phe Arg Gly Val Gln Glu Met Phe Asp Asp Cys Val Gln Ser Leu Lys  
305 310 315 320

Asp Gln Gly His Leu Leu Glu Cys Pro Leu  
325 330

<210> 3

<211> 2544

<212> DNA

<213> Zea mays

<400> 3

```

gaattctcgt ctcggcgggtc aactgaaccg taaacagtgg aaagtggata ctctttctct 60
ctctgcaatc cgtgccgtgg aagcaaatgg cgcagtcgcc tacttatcac accaacttat 120
cacctagaaa agcgacgcgt cctggatcga ttgcaaatct acctccaacc aaccagctt 180
tgtatctgct tactgtgata accaaagtgt tgctgatacg atgtgcgatt attgctcttt 240
cttctctaga atgttcctgc cgatgcttta taagagaagg ttggtcagca tcgatctctg 300
ccagtgtcta gctgagaaca tggtagacct aagcaagggc aaggtagcg taaccggggc 360
ctcaggcttt gttgcctctt ggcttatcaa acggctcctc gagtctggat atcatgtggt 420
agggactgtc agggacccag gtatttgcca aatatcatta ctatcgatc agtcctcttt 480
attacattaa taattcttga ttaccaattt tttctttttt ttttttggt acccacaagg 540
aatcaccaa aagacagccc acctttggaa attacctggc gctaaagaga ggctgcaaat 600
cgtgcgagct gatctgttgg aagaagggag cttcgacagc gccgtgatgg cctgtgaggg 660
tgtattccac actgcatccc cgtcctcgc taaaccgcac tctactagca aggcattgcca 720
tcgccgcata tatatatgca tatctggacc atgcatacta ctgcagcctt ttctatacgg 780
aagcgcgttg catctaccgt acgtgaagct agctatctaa gctaagctgt ttttcatgca 840
tgcattggtc agggaggacac gctcgtccct gcggtgaacg gtactctgaa cgtgctgaga 900
tcgtgcaaga agaaccgcgt cctgaaaagg gtcgtcctta cgtcttcgtc gtctgcggtg 960
aggatcaggg acgacggtgg ccagtcaggt aacatctcgc tggacgaaac gacatggagc 1020
tcctgcccac tctgcgagaa gatgcatgtg agatactact gaacagtgtc tactctctct 1080
ctctctgtca tcgatctcaa accgtgatct gaaaaacacg catgcgcgca caggttgccg 1140
tcgtcgtccc tttgtgtgtt caccggaagc tatggtatgc cctagccaag gtatttgca 1200
agaaagcggc gtgggagttc gccaaaggaga acggcatcga ccttgtgact gtcctcccg 1260
cgttcgtgat cgggcccggt ttgtcccacg aactatgcgt taccgcttca gacgtcctag 1320
gcctattcca aggtattcat ctcaatcatt grbcgtacgt gttctgggtt tcgtatgta 1380
aatagatgac tggaaacaag aggtatacat atatatactc tctgttcctc ccccccccc 1440
ccccccaccc ccaggcgaca cggcaagggt cagctcgtac ggaagaatgg ggtacgtcca 1500
catcgacgac gttgcgagca gccacatcct ggtgtacgag gccccccagg ccgccgggag 1560
gtacctgtgc agctcagtggt tgctggacaa cgacgagctg gtctcctcgc tcgcgaaacg 1620
ctaccgata ttccccatac cccggagggt agtcgtcgtc gcgtcgtctg gatgtgcgtg 1680
ccattttaag atctctgaac gggagagccg tgtgcatggt ccgttctgct gcagctgaa 1740
cagccccctac ggcaagcagt cgtaccagct gaacacgtcg aagctgcagg ggctgggctt 1800
caagttcaga ggggtgcagg agatgttcga cgactgcgta cagtcgtca aagaccaggg 1860
acacctgctg gagtgcctcc tgtgaactgc gatggggtgc ctccgcctgt gaacgcgccg 1920
gttgggttgc gtcccgaaac cgctgttaat tcgtttttt ttcttcaata attccacgtc 1980

```

```

atgtcacggt gtcctcgcgc agactgctac tgtcagggcg tcatagctca cgggctctcc 2040
ggctacatga ataaaaatgt cacgctcgtc atttgctttg cttttttttt tgggttcggt 2100
ctgcgaactt ccgttcgctg tgtgtacttg tggctgccgg tcgccttgtc ggtgtggcga 2160
ctgatgatgg tgatcggagg caggcacccg tgtgtgcgtg cgatcaaccg aacgccatgt 2220
ggcgggtttg atggacgaat ggctccacca tcgatctgag tcattcggat tttgaaccgc 2280
tgatttgtcc actggacggc actagcatca agattcagtc tcaaatccca aattcctcaa 2340
cgcaaagcca caaagagaga atgaatgtac agtgtttcaa gccacagctc actagctcaa 2400
aagtagtgag catgcacacc tgtattttaca tgcatgcatg tacaccccca ccccactac 2460
ttgtacactt tgtaaaccaa ccaaccaacc aaccaagcaa gcaatcaagc aaacacacag 2520
agcaaaccgt acgtggctgg cgcc                                     2544

```

<210> 4

<400> 4

000

<210> 5

<211> 322

<212> DNA

<213> Zea mays

<400> 5

```

gaattctcgt ctcggcggtc aactgaaccg taaacagtgg aaagtggata ctctttctct 60
ctctgcaatc cgtgccgtgg aagcaaatgg cgcagtcgcc tacttatcac accaacttat 120
cacctagaaa agcgacgcgt cctggatcga ttgcaaattc acctccaacc aaccagctt 180
tgtatctgct tactgtgatc accaaagttg tgctgatacg atgtgcgatt attgctcttt 240
cttctctaga atgttcctgc cgatgcttta taagagaagg ttggtcagca tcgatctctg 300
ccagtgtcta gctgagaaca tg                                     322

```

<210> 6

<211> 187

<212> DNA

<213> Zea mays

<400> 6

```

cggtcctcgt atcgattgca aatctacctc caaccaaccc agctttgtat ctgcttactg 60
tgatcaccaa agttgtgctg atacgatgtg cgattattgc tctttcttct ctagaatgtt 120
cctgccgatg ctttataaga gaaggttggt cagcatcgat ctctgccagt gtctagctga 180
gaacatg                                     187

```

<210> 7

<211> 697

<212> DNA

<213> Sorghum sp.

<220>

<221> CDS

<222> (1)..(696)

<400> 7

```

gta acc ggg gct tca ggc ttt att gcc tct tgg ctt atc aaa cgg ctg 48
Val Thr Gly Ala Ser Gly Phe Ile Ala Ser Trp Leu Ile Lys Arg Leu
1 5 10 15

```

ctc gag tct gga tat cat gtg gta ggg act gtc aga gac cca gga aat	96
Leu Glu Ser Gly Tyr His Val Val Gly Thr Val Arg Asp Pro Gly Asn	
20 25 30	
cac caa aaa aca gca cac ctt tgg aaa tta cct ggt gcc aaa gag agg	144
His Gln Lys Thr Ala His Leu Trp Lys Leu Pro Gly Ala Lys Glu Arg	
35 40 45	
ctg caa att gtg cga gct gat ctg ttg gaa gaa ggg agc ttt gac aat	192
Leu Gln Ile Val Arg Ala Asp Leu Leu Glu Glu Gly Ser Phe Asp Asn	
50 55 60	
gct gtc atg gac tgt gat ggc gtc ttc cac act gca tcc cct gtg ctc	240
Ala Val Met Asp Cys Asp Gly Val Phe His Thr Ala Ser Pro Val Leu	
65 70 75 80	
gct aaa tct gat tct agt agc aag gag gaa acg ctt tgt cca gca gta	288
Ala Lys Ser Asp Ser Ser Ser Lys Glu Glu Thr Leu Cys Pro Ala Val	
85 90 95	
aac ggt act ctg aat gtg cta aga tcg tgc aag aag aac cca ttt ctg	336
Asn Gly Thr Leu Asn Val Leu Arg Ser Cys Lys Lys Asn Pro Phe Leu	
100 105 110	
aaa agg gtt gtt ctt acg tct tca tca tct gca gtg agg att agg gat	384
Lys Arg Val Val Leu Thr Ser Ser Ser Ser Ala Val Arg Ile Arg Asp	
115 120 125	
gat gat cag cct aat atc tca ctg gat gaa aca aca tgg agc tct gtg	432
Asp Asp Gln Pro Asn Ile Ser Leu Asp Glu Thr Thr Trp Ser Ser Val	
130 135 140	
cca ctc tgt gaa aag atg cag cta tgg tat gcc cta gcg aag gta ttt	480
Pro Leu Cys Glu Lys Met Gln Leu Trp Tyr Ala Leu Ala Lys Val Phe	
145 150 155 160	
gca gag aaa gcg gca tgg gaa ttc gcc aag gag aac aac atc gac ctt	528
Ala Glu Lys Ala Ala Trp Glu Phe Ala Lys Glu Asn Asn Ile Asp Leu	
165 170 175	
gtg act gtc ctc cca tca ttt gtg atc ggg ccc agt tta tcc cat gaa	576
Val Thr Val Leu Pro Ser Phe Val Ile Gly Pro Ser Leu Ser His Glu	
180 185 190	
cta tgt gtt acc gct tca gat gtc cta ggc tta ttc caa ggt gac acg	624
Leu Cys Val Thr Ala Ser Asp Val Leu Gly Leu Phe Gln Gly Asp Thr	
195 200 205	
gca agg ttc agt tct tac gga aga atg gga tac gtt cac atc gac gat	672
Ala Arg Phe Ser Ser Tyr Gly Arg Met Gly Tyr Val His Ile Asp Asp	
210 215 220	
gtt gcg acc agc cac atc ctg gtg t	697
Val Ala Thr Ser His Ile Leu Val	
225 230	

[illegible]